

John

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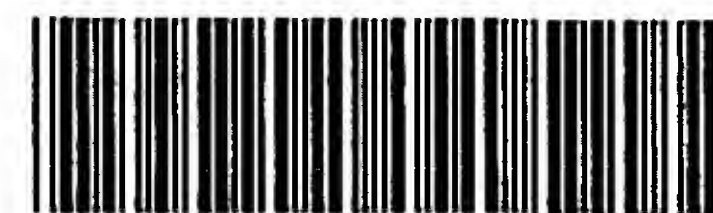
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/532,605

Source: P4/10

Date Processed by STIC: 11/16/05

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/532,605

DATE: 11/16/2005

TIME: 08:18:02

Input Set : A:\Q87625.ST25.txt

Output Set: N:\CRF4\11162005\J532605.raw

3 <110> APPLICANT: Miwa, Takehiro
 5 <120> TITLE OF INVENTION: Method for digesting proteins highly resistant to
 denaturation
 6 and degradation
 8 <130> FILE REFERENCE: Q87625
 10 <140> CURRENT APPLICATION NUMBER: US 10/532,605
 C--> 11 <141> CURRENT FILING DATE: 2005-04-25
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/013658
 14 <151> PRIOR FILING DATE: 2003-10-24
 16 <160> NUMBER OF SEQ ID NOS: 4
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 825
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Bacillus Licheniformis
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(825)
 30 <400> SEQUENCE: 1
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 32 Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
 33 1 5 10 15
 35 cag gcc caa ggt tat aaa ggg gca aat gtc aaa gtc ggt atc att gat 96
 36 Gln Ala Gln Gly Tyr Lys Gly Ala Asn Val Lys Val Gly Ile Ile Asp
 37 20 25 30
 39 acg gga atc gct tcg tct cat aca gac ttg aag gta gtc ggc gga gca 144
 40 Thr Gly Ile Ala Ser Ser His Thr Asp Leu Lys Val Val Gly Gly Ala
 41 35 40 45
 43 agc ttt gta tct ggt gaa agt tat aat acg gac ggt aac gga cac ggc 192
 44 Ser Phe Val Ser Gly Glu Ser Tyr Asn Thr Asp Gly Asn Gly His Gly
 45 50 55 60
 47 aca cat gtt gcc gga aca gtg gcg gcg ctt gac aat aca aca ggc gtt 240
 48 Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
 49 65 70 75 80
 51 tta ggc gtt gca ccg aac gtc tcc ctc tac gcg att aag gtg ttg aat 288
 52 Leu Gly Val Ala Pro Asn Val Ser Leu Tyr Ala Ile Lys Val Leu Asn
 53 85 90 95
 55 tca agc gga agc gga aca tac agc gca atc gtc agc gga att gag tgg 336
 56 Ser Ser Gly Ser Gly Thr Tyr Ser Ala Ile Val Ser Gly Ile Glu Trp
 57 100 105 110
 59 gcc aca caa aac ggc ctg gat gtc atc aac atg agc ctc ggc gga cca 384
 60 Ala Thr Gln Asn Gly Leu Asp Val Ile Asn Met Ser Leu Gly Gly Pro
 61 115 120 125
 63 tcc ggc tca act gcg ctg aaa cag gct gtg gat aaa gca tat gcc agc 432

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64 Ser Gly Ser Thr Ala Leu Lys Gln Ala Val Asp Lys Ala Tyr Ala Ser
65      130                      135                      140
67 gga att gtc gta gtg gca gca gcg ggg aac agc gga tct tcc ggc agc      480
68 Gly Ile Val Val Val Ala Ala Ala Gly Asn Ser Gly Ser Ser Gly Ser
69 145                      150                      155                      160
71 caa aac aca atc ggc tat ccg gca aaa tat gac tcc gtc atc gcc gtc      528
72 Gln Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
73                      165                      170                      175
75 ggt gcg gtt gac agc aac aaa aac aga gct tca ttc tcc agc gtc ggc      576
76 Gly Ala Val Asp Ser Asn Lys Asn Arg Ala Ser Phe Ser Ser Val Gly
77                      180                      185                      190
79 tca gag ctt gaa gtc atg gct cct ggc gtc agc gta tac agc aca tat      624
80 Ser Glu Leu Glu Val Met Ala Pro Gly Val Ser Val Tyr Ser Thr Tyr
81                      195                      200                      205
83 cct tct aac acg tac aca tca ttg aac gga act tca atg gct tcg cct      672
84 Pro Ser Asn Thr Tyr Thr Ser Leu Asn Gly Thr Ser Met Ala Ser Pro
85      210                      215                      220
87 cat gta gcg gga gca gca gcc ttg atc ttg tcg aaa tac cct acg ctt      720
88 His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys Tyr Pro Thr Leu
89 225                      230                      235                      240
91 tca gct tcc caa gtt cgc aac cgc ctc tca agc act gcg act aat ttg      768
92 Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Asn Leu
93                      245                      250                      255
95 gga gat tcc ttc tac tac ggc aaa ggg ctg atc aat gta gaa gct gcc      816
96 Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
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99 gct caa taa      825
100 Ala Gln
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105 <211> LENGTH: 274
106 <212> TYPE: PRT
107 <213> ORGANISM: Bacillus Licheniformis
109 <400> SEQUENCE: 2
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116      20                      25                      30
119 Thr Gly Ile Ala Ser Ser His Thr Asp Leu Lys Val Val Gly Gly Ala
120      35                      40                      45
123 Ser Phe Val Ser Gly Glu Ser Tyr Asn Thr Asp Gly Asn Gly His Gly
124      50                      55                      60
127 Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
128 65                      70                      75                      80
131 Leu Gly Val Ala Pro Asn Val Ser Leu Tyr Ala Ile Lys Val Leu Asn
132      85                      90                      95
135 Ser Ser Gly Ser Gly Thr Tyr Ser Ala Ile Val Ser Gly Ile Glu Trp
136      100                     105                     110
139 Ala Thr Gln Asn Gly Leu Asp Val Ile Asn Met Ser Leu Gly Gly Pro
140      115                     120                     125

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143 Ser Gly Ser Thr Ala Leu Lys Gln Ala Val Asp Lys Ala Tyr Ala Ser
144      130                      135                      140
147 Gly Ile Val Val Val Ala Ala Ala Gly Asn Ser Gly Ser Ser Gly Ser
148 145                      150                      155                      160
151 Gln Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
152                      165                      170                      175
155 Gly Ala Val Asp Ser Asn Lys Asn Arg Ala Ser Phe Ser Ser Val Gly
156                      180                      185                      190
159 Ser Glu Leu Glu Val Met Ala Pro Gly Val Ser Val Tyr Ser Thr Tyr
160      195                      200                      205
163 Pro Ser Asn Thr Tyr Thr Ser Leu Asn Gly Thr Ser Met Ala Ser Pro
164      210                      215                      220
167 His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys Tyr Pro Thr Leu
168 225                      230                      235                      240
171 Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Asn Leu
172                      245                      250                      255
175 Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
176      260                      265                      270

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179 Ala Gln

183 <210> SEQ ID NO: 3

184 <211> LENGTH: 20

185 <212> TYPE: DNA

186 <213> ORGANISM: Artificial Sequence

188 <220> FEATURE:

189 <223> OTHER INFORMATION: Chemically - synthesized Primer PDE-2

191 <400> SEQUENCE: 3

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195 <210> SEQ ID NO: 4

196 <211> LENGTH: 20

197 <212> TYPE: DNA

198 <213> ORGANISM: Artificial Sequence

200 <220> FEATURE:

201 <223> OTHER INFORMATION: Chemically-synthesized Primer PDE-5

203 <400> SEQUENCE: 4

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/532,605

DATE: 11/16/2005

TIME: 08:18:03

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Output Set: N:\CRF4\11162005\J532605.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date